In the Claims:

Please replace the claims with the following listings of claims:

1. to 5. (Canceled).

6. (Currently Amended) A diagnostic system for quantitating the individual contribution of a mutation or combination of mutations to a drug resistance phenotype exhibited by an HIV strain, said system comprising

means for obtaining a genetic sequence of said HIV strain;

means for identifying the mutation pattern in said genetic sequence as compared to wild type HIV; and

means for predicting the fold resistance exhibited by said HIV strain ~~A method for quantitating the individual contribution of a mutation or combination of mutations to a drug resistance phenotype exhibited by HIV, said~~ using a method comprising the steps of:

1~~a~~) performing a linear regression analysis using data from a dataset of matching genotypes and phenotypes, wherein the log fold resistance, pFR, of each said HIV strain is modeled ~~modelled~~ as the sum of all the individual resistance contributions for each of said mutations or combinations of mutations that occur in HIV according to the following equation;

$$pFR = \beta_A M_A + \beta_B M_B + \beta_n M_n + \cdots + \beta_Z M_Z + \varepsilon$$

wherein each said individual resistance contribution is calculated by multiplying a mutation factor, M_A , M_B , ..., M_Z, for each of said mutation or combination of mutations by a resistance coefficient β_A, β_B, ..., β_Z;

wherein for a combination of mutations, said ~~the~~ mutation factor M_n represents the co-occurrence of one mutation with other one or more mutations and said ~~the~~ coefficient β_n represents the synergy or antagonism between said ~~the~~ one mutation with said ~~the~~ other one or more mutations;

wherein said ~~the~~ mutation factor assigned to each said mutation or combination of mutations reflects the degree to which said mutation or combination of mutations is present in said HIV strain and, if present, to which degree said ~~the~~ mutation is present in a mixture;

wherein each said resistance coefficient reflects the contribution of said ~~the~~ mutation or combination of mutations to said ~~the~~ fold resistance exhibited by said strain;

wherein the error term ε, represents the difference between a modeled ~~modelled~~ prediction and an experimentally determined measurement;

2) replacing ~~wherein~~ the censored values in said data from said dataset of matching genotype and/~~-~~phenotype ~~database are replaced~~ by a maximum likelihood estimation;

wherein for each iteration of said linear regression, said maximum likelihood estimation is generated according to the following steps:

~~wherein for each iteration of the linear regression, the following steps are performed until the predictions converge:~~

a) calculating a linear regression model without said censored values;

b) using a phenotypic measured value V_0 of said data of said dataset of matching genotypes and phenotypes as if the censor was " = ", when a result is expressed as $-\log FR < 4$, V_0 is treated as $-\log FR = 4$;

c) using ~~looking at~~ the prediction P from ~~the~~said linear regression model to ~~and~~ apply either:

When said phenotypic value is smaller than said range, ~~ease~~ a '<'-censor is applied to said value:

i) $P < V_0 - 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove value from training data for the next iteration

ii) $V_0 - 0.798\ \sigma \leq P < V_0$

Use $V' = V_0 - 0.798\ \sigma$ for the next iteration

iii) $V_0 \leq P$

Use V' center ~~centre~~ of gravity of tail (<V) of a normal distribution N (P, σ) as value for the next iteration

When said phenotypic value is higher than said range, ~~ease~~ a '>'-censor is applied to said value:

i) $P > V_0 + 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove value from training data for the next iteration

ii) $V_0 + 0.798\ \sigma \geq P > V_0$

Use $V' = V_0 - 0.798\ \sigma$ for the next iteration

iii) $V_0 \geq P$

Use V' center ~~centre~~ of gravity of tail (>V) of a normal distribution N (P, σ) as value for the next iteration;

d) calculating a linear regression model and for said ~~the~~ censored values in said ~~the~~ linear regression model, either remove the data-point from the training set, or use V' instead of the censored phenotypes measurement, as described in step c);

e) reiterating ~~from~~ steps b) to d) until the prediction converges;

thereby quantitating the individual contribution of said mutation or combination of mutations to said~~a~~ drug resistance phenotype exhibited by said HIV strain.

7. to 16. (Canceled).